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Sequence Listing was accepted.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866)  
217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2007; month=11; day=28; hr=18; min=49; sec=34; ms=540;  
]

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Application No: 09776874 Version No: 3.1

Input Set:

Output Set:

**Started:** 2007-11-28 18:48:15.849  
**Finished:** 2007-11-28 18:48:19.043  
**Elapsed:** 0 hr(s) 0 min(s) 3 sec(s) 194 ms  
**Total Warnings:** 32  
**Total Errors:** 3  
**No. of SeqIDs Defined:** 47  
**Actual SeqID Count:** 47

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
E 201	Mandatory field data missing in <223> in SEQ ID (11)
E 201	Mandatory field data missing in <223> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20)
W 213	Artificial or Unknown found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)

**Input Set:**

**Output Set:**

**Started:** 2007-11-28 18:48:15.849  
**Finished:** 2007-11-28 18:48:19.043  
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**Total Warnings:** 32  
**Total Errors:** 3  
**No. of SeqIDs Defined:** 47  
**Actual SeqID Count:** 47

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (28)
W 213	Artificial or Unknown found in <213> in SEQ ID (29) This error has occurred more than 20 times, will not be displayed
E 201	Mandatory field data missing in <223> in SEQ ID (45)

# SEQUENCE LISTING

<110> Pecker, Iris  
Vlodavsky , Israel  
Feinstein, Elena

<120> POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE ACTIVITY  
AND EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS

<130> 01/22603

<140> 09776874

<141> 2001-02-06

<150> US 08/922,170

<151> 1997-09-02

<150> US 09/109,386

<151> 1998-07-10

<150> PCT/US98/17954

<151> 1998-08-31

<160> 47

<170> PatentIn version 3.1

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<210> 9

<211> 1721

<212> DNA

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Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro  
 35 40 45

Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn  
 50 55 60

Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu  
 65 70 75 80

Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly  
 85 90 95

Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe  
 100 105 110

Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys  
 115 120 125

Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp  
130 135 140

Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys Phe  
145 150 155 160

Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe  
165 170 175

Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu  
180 185 190

Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu  
195 200 205

Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn  
210 215 220

Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly Ser  
225 230 235 240

Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys Ser  
245 250 255

Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro Arg  
260 265 270

Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly Glu  
275 280 285

Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg Thr  
290 295 300

Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe Ile  
305 310 315 320

Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro Gly  
325 330 335

Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly Ala  
340 345 350

Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp Lys



355

360

365

Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln Val  
370 375 380

Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp Pro  
385 390 395 400

Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly Thr  
405 410 415

Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu Arg  
420 425 430

Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu Gly  
435 440 445

Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr Leu  
450 455 460

Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu Leu  
465 470 475 480

Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu Asn  
485 490 495

Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu Met  
500 505 510

Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe Ser  
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Tyr Ser Phe Phe Val Ile Arg Asn Ala Lys Val Ala Ala Cys Ile  
530 535 540

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&lt;211&gt; 1721

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (63)..(1691)

&lt;223&gt;

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Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg	
20 25 30	
cct gcg caa gca cag gac gtc gtg gac ctg gac ttc ttc acc cag gag	203
Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu	
35 40 45	
ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc	251
Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala	
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aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag	299
Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys	
65 70 75	
ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt	347
Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly	
80 85 90 95	
ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc	395
Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr	
100 105 110	
ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc	443
Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys	
115 120 125	
aaa tat gga tcc atc cct cct gat gtg gag gag aag tta cgg ttg gaa	491
Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu	
130 135 140	
tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag	539
Trp Pro Tyr Gln Glu Gln Leu Leu Leu Arg Glu His Tyr Gln Lys Lys	
145 150 155	
ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act	587
Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr	
160 165 170 175	
ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta	635
Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu	
180 185 190	
tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc	683
Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu	
195 200 205	
ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc	731

Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly	
210 215 220	
aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg	779
Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly	
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tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag	827
Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys	
240 245 250 255	
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Ser Thr Phe Lys Asn Ala Lys Leu Tyr Gly Pro Asp Val Gly Gln Pro	
260 265 270	
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Arg Arg Lys Thr Ala Lys Met Leu Lys Ser Phe Leu Lys Ala Gly Gly	
275 280 285	
gaa gtg att gat tca gtt aca tgg cat cac tac tat ttg aat gga cgg	971
Glu Val Ile Asp Ser Val Thr Trp His His Tyr Tyr Leu Asn Gly Arg	
290 295 300	
act gct acc agg gaa gat ttt cta aac cct gat gta ttg gac att ttt	1019
Thr Ala Thr Arg Glu Asp Phe Leu Asn Pro Asp Val Leu Asp Ile Phe	
305 310 315	
att tca tct gtg caa aaa gtt ttc cag gtg gtt gag agc acc agg cct	1067
Ile Ser Ser Val Gln Lys Val Phe Gln Val Val Glu Ser Thr Arg Pro	
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Gly Lys Lys Val Trp Leu Gly Glu Thr Ser Ser Ala Tyr Gly Gly Gly	
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Ala Pro Leu Leu Ser Asp Thr Phe Ala Ala Gly Phe Met Trp Leu Asp	
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aaa ttg ggc ctg tca gcc cga atg gga ata gaa gtg gtg atg agg caa	1211
Lys Leu Gly Leu Ser Ala Arg Met Gly Ile Glu Val Val Met Arg Gln	
370 375 380	
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Val Phe Phe Gly Ala Gly Asn Tyr His Leu Val Asp Glu Asn Phe Asp	
385 390 395	
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Pro Leu Pro Asp Tyr Trp Leu Ser Leu Leu Phe Lys Lys Leu Val Gly	
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acc aag gtg tta atg gca agc gtg caa ggt tca aag aga agg aag ctt	1355
Thr Lys Val Leu Met Ala Ser Val Gln Gly Ser Lys Arg Arg Lys Leu	
420 425 430	
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Arg Val Tyr Leu His Cys Thr Asn Thr Asp Asn Pro Arg Tyr Lys Glu	

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Gly Asp Leu Thr Leu Tyr Ala Ile Asn Leu His Asn Val Thr Lys Tyr			
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ttg cgg tta ccc tat cct ttt tct aac aag caa gtg gat aaa tac ctt			1499
Leu Arg Leu Pro Tyr Pro Phe Ser Asn Lys Gln Val Asp Lys Tyr Leu			
465	470	475	
cta aga cct ttg gga cct cat gga tta ctt tcc aaa tct gtc caa ctc			1547
Leu Arg Pro Leu Gly Pro His Gly Leu Leu Ser Lys Ser Val Gln Leu			
480	485	490	495
aat ggt cta act cta aag atg gtg gat gat caa acc ttg cca cct tta			1595
Asn Gly Leu Thr Leu Lys Met Val Asp Asp Gln Thr Leu Pro Pro Leu			
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Met Glu Lys Pro Leu Arg Pro Gly Ser Ser Leu Gly Leu Pro Ala Phe			
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